**Amendments to the Specification**

Please replace the paragraph on page 4, lines 6-12 with the following amended paragraph:

-- **Fig. 1.** shows the nucleotide sequence **(SEQ ID NO: 1)** and deduced amino acid sequence **(SEQ ID NO: 2)** of *rdxA* of WT strain 500. The Shine-Dalgarno (SD) ribosome-binding site is underlined on the nucleotide sequence. The underlined amino acid sequence defines a highly conserved region among classic nitroreductase (CNR) proteins. Cysteine residues are highlighted in bold face and the *Sph*1 sites used for insertion of the *camR* cassette are underlined and noted. ***H. pylori* strains 439 and 1107 contain transition substitutions (TT for CC). --

Please replace the paragraph on page 4, lines 13-19 with the following amended paragraph:

-- **Fig. 2.** indicates the location of amino acid substitutions in RdxA from matched $Mtz^{R/S}$ strains and from clinical isolates **(SEQ ID NOS 23 & 3-18, respectively, in order of appearance)**. *H. pylori* strain 1107 was created by transforming DNA from $Mtz^{R}$ strain 439 into $Mtz^{S}$ strain 500. Note that the RdxA amino acid sequence is identical, indicating allelic exchange recombination occurred outside the *rdxA* locus. Other clinical isolates are included for comparison. The five matched pairs of isolates are grouped separately and the amino acid substitutions are listed in Table 3. --

Please replace the paragraph on page 5, lines 13-26 with the following amended paragraph:

-- In accordance with another aspect of the present invention, there are provided nitroreductases further characterized as being encoded by DNA having greater than about 90% homology with the *H. pylori rdxA* gene (see SEQ ID NO:1 and Fig. 1). Preferably, invention nitroreductases contain a conserved amino acid motif common to the CNRs (QPWHF) **(residues 50-54 of SEQ ID NO: 2)** as well as the positioning of a strategic cysteine residue (position 87, see SEQ ID NO:2). In a more preferred aspect of this embodiment, invention nitroreductases are isolated from microaerophilic bacterial species such as *Helicobacter*, *Campylobacter*, and the like. An especially preferred nitroreductase is the *H. pylori* nitroreductase (RdxA) and homologues thereof. Those of skill in the art will readily recognize that similar nitroreductases can be isolated from other *Helicobacter* species, including, *H. acinonyx, H. bilis, H. bizzozeronii, H. canis, H. cholecystus, H. cinaedi, H. felis, H. fennelli, H. heilmanni, H. hepaticus, H. muridarum, H. mustelae, H. nemestrenae, H. pullorum, H. rodentium, H. salamonis, H. suncus, H. trogontum*, and the like. The presently preferred nitroreductase is the RdxA of *H. pylori* strain HP950. --

Please replace the paragraph on page 17, line 14, through page 18, line 4 with the following amended paragraph:

-- The WT *rdxA* gene was 630bp in length and had a Shine-Dalgarno sequence 5bp upstream of the start codon. The CNR proteins of the enteric bacteria are acidic proteins, including HP0642 ('*frxA*')(pI = 5.4-5.6), and generally contain one to two cysteine residues. However, RdxA is a basic protein (pI = 7.99) and contains six cysteine residues. One of the cysteine residues (position 87) is conserved in the CNR proteins of the enterics. The cysteine located at position 159 is in a motif (L/IDSCI/PI)**(SEQ ID NO: 22)** shared with the inferred product of *frxA*. Another motif common to all of the CNRs is QPWHF **(SEQ ID NO: 21)** (PW is absolutely conserved) located within a highly conserved region between positions 43-59 in RdxA. --

Please replace the paragraph on page 21, lines 16-23 with the following amended paragraph:

-- To assess how often $Mtz^R$ is acquired by *de novo* mutation vs. *rdxA* gene transfer from an unrelated strain that is already MtzR, *rdxA* genes from infections that were mixed with respect to $Mtz^R/Mtz^S$, and in which the $Mtz^R$ and $Mtz^S$ isolates seemed to be very closely related based on arbitrarily primed PCR cloning/sequencing have been studied. *rdxA* sequences from various strains of *H. pylori* were amplified and cloned into pBluescript using primer pairs Mtz6EF (forward) 5' – TGAATTCGAGCATGGGGCAG **(SEQ ID NO: 19)** and reverse primer $Mtz^R$Bgl 5'-AGCAGGAGCATCAGATAGATCTGA~~DNA~~ **(SEQ ID NO: 20)**. --